

RAW SEQUENCE LISTING ERROR REPORT

(Faxed)
The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/265,540A

Art Unit / Team No.: 1646

Date Processed by STIC: 6/9/2000

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**
- 2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/265,540A

 DATE: 06/09/2000
 TIME: 20:51:34

Input Set: I265540A.RAW

This Raw Listing contains the General Information Section and up to first 5 pages.

 Does Not Comply
 Corrected Diskette Needed

1 <110> APPLICANT: Parham, Christi L.
 2 Moore, Kevin W.
 3 Murgolo, Nicholas J.
 4 Bazan, J. Fernando
 5 <120> TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
 6 <130> FILE REFERENCE: DX0804
 7 <140> CURRENT APPLICATION NUMBER: US/09/265,540A
 8 <141> CURRENT FILING DATE: 1999-03-08
 9 <160> NUMBER OF SEQ ID NOS: 6
 10 <170> SOFTWARE: PatentIn Ver. 2.0
 11 <210> SEQ ID NO 1
 12 <211> LENGTH: 1381
 13 <212> TYPE: DNA
 14 <213> ORGANISM: primate
 15 <220> FEATURE:
 16 <221> NAME/KEY: CDS
 17 <222> LOCATION: (132)..(1064) *p. 2*
 18 <220> FEATURE:
 19 <221> NAME/KEY: misc_feature
 20 <222> LOCATION: n at position 567 and 573 *where don't n; at locations* 1336, 1342, 1369?
 21 <223> OTHER INFORMATION: n may be A, C, T, or G; translated amino acid depends on g
 22 <400> SEQUENCE: 1
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 gagtctacca a atg cag act ttc aca atg gtt cta gaa gaa atc tgg aca 170
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 1 5 10
 agt ctt ttc atg tgg ttt ttc tac gca ttg att cca tgt ttg ctc aca 218
 Ser Leu Phe Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr
 15 20 25
 gat gaa gtg gcc att ctg cct gcc cct cag aac ctc tct gta ctc tca 266
 Asp Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser
 30 35 40 45
 acc aac atg aag cat ctc ttg atg tgg agc cca gtg atc gcg cct gga 314
 Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly
 50 55 60
 gaa aca gtg tac tat tct gtc gaa tac cag ggg gag tac gag agc ctg 362
 Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu
 65 70 75
 tac acg agc cac atc tgg atc ccc agc agc tgg tgc tca ctc act gaa 410
 Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu
 80 85 90
 ggt cct gag tgt gat gtc act gat gac atc acg gcc act gtg cca tac 458
 Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr

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45 95 100 105
 46 aac ctt cgt gtc agg gcc aca ttg ggc tca cag acc tca gcc tgg agc 506
 47 Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser
 48 110 115 120 125
 49 atc ctg aag cat ccc ttt aat aga aac tca acc atc ctt acc cga cct 554
 50 Ile Leu Lys His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro
 51 130 135 140
 52 ggg atg gag atc ncc aaa nat ggc ttc cac ctg gtt att gag ctg gag 602
 53 Gly Met Glu Ile Xaa Lys Xaa Gly Phe His Leu Val Ile Glu Leu Glu
 54 145 150 155
 55 gac ctg ggg ccc cag ttt gag ttc ctt gtg gcc tac tgg asg agg gag 650
 56 Asp Leu Gly Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Xaa Arg Glu
 57 160 165 170
 58 cct ggt gcc gag gaa cat gtc aaa atg gtg agg agt ggg ggt att cca 698
 59 Pro Gly Ala Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro
 60 175 180 185
 61 gtg cac cta gaa acc atg gag cca ggg gct gca tac tgt gtg aag gcc 746
 62 Val His Leu Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala
 63 190 195 200 205
 64 cag aca ttc gtg aag gcc att ggg arg tac agc gcc ttc agc cag aca 794
 65 Gln Thr Phe Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe Ser Gln Thr
 66 210 215 220
 67 gaa tgt gtg gar gtg caa gga gag gcc att ccc ctg gta ctg gcc ctg 842
 68 Glu Cys Val Xaa Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu
 69 225 230 235
 70 ttt gcc ttt gtt ggc ttc atg ctg atc ctt gtg gtc gtg cca ctg ttc 890
 71 Phe Ala Phe Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe
 72 240 245 250
 73 gtc tgg aaa atg ggc cgg ctg ctc cag tac tcc tgt tgc ccc gtg gtg 938
 74 Val Trp Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val
 75 255 260 265
 76 gtc ctc cca gac acc ttg aaa ata acc aat tca ccc cag aag tta atc 986
 77 Val Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile
 78 270 275 280 285
 79 agc tgc aga agg gag gag gtg gat gcc tgt gtc acg gct gtg atg tct 1034
 80 Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser
 81 290 295 300
 82 cct gag gaa ctc ctc agg gcc tgg atc tca taggtttgcg gaaggccc 1084
 83 Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser
 84 305 310
 85 ggtgaagccg agaaccttgtt ctgcatacata tggaaaccat gaggggacaa gttgttttc 1144
 86 tgtttccgc cacggacaag ggatgagaga agtaggaaga gcctgttgc tacaagtcta 1204
 87 gaagcaacca tcagaggcag ggtgtttgt ckaacagaac aaytgactga ggytakrggg 1264
 88 gwtgtacact cttagactktg ggstkscayt tgcwtggytg agcaaccctg ggaaaagtga 1324
 89 cttcatccct tgggtccaa gttttctcat ctgtaatggg ggatnctac aaaactg 1381
 90 <210> SEQ ID NO 2
 91 <211> LENGTH: 311
 92 <212> TYPE: PRT
 93 <213> ORGANISM: primate
 94 <220> FEATURE:

W-->

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/265,540A

 DATE: 06/09/2000
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Input Set: I265540A.RAW

95 <221> NAME/KEY: misc_feature
 96 <222> LOCATION: Xaa at residues 146, 148, 171, 214 and 225
 97 <223> OTHER INFORMATION: Xaa depends on corresponding codon
 98 <400> SEQUENCE: 2
 99 Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr Ser Leu Phe
 100 1 5 10 15
 101 Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr Asp Glu Val
 102 20 25 30
 103 Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser Thr Asn Met
 104 35 40 45
 105 Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly Glu Thr Val
 106 50 55 60
 107 Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu Tyr Thr Ser
 108 65 70 75 80
 109 His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu Gly Pro Glu
 110 85 90 95
 111 Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr Asn Leu Arg
 112 100 105 110
 113 Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser Ile Leu Lys
 114 115 120 125
 115 His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro Gly Met Glu
 116 130 135 140
 W--> 117 Ile Xaa Lys Xaa Gly Phe His Leu Val Ile Glu Leu Glu Asp Leu Gly
 118 145 150 155 160
 W--> 119 Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Xaa Arg Glu Pro Gly Ala
 120 165 170 175
 121 Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu
 122 180 185 190
 123 Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe
 124 195 200 205
 W--> 125 Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val
 126 210 215 220
 W--> 127 Xaa Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe
 128 225 230 235 240
 129 Val Gly Phe Met Leu Ile Leu Val Val Pro Leu Phe Val Trp Lys
 130 245 250 255
 131 Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Val Leu Pro
 132 260 265 270
 133 Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile Ser Cys Arg
 134 275 280 285
 135 Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser Pro Glu Glu
 136 290 295 300
 137 Leu Leu Arg Ala Trp Ile Ser
 138 305 310
 139 <210> SEQ ID NO 3
 140 <211> LENGTH: 1244
 141 <212> TYPE: DNA
 142 <213> ORGANISM: primate
 143 <220> FEATURE:
 144 <221> NAME/KEY: CDS

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RAW SEQUENCE LISTING
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 149 1 5 10 15
 150 tgg ttc ctg tcc tgt tgg aat gtt acc att ggg cct cct gag agc atc 97
 151 Trp Phe Leu Ser Cys Trp Asn Val Thr Ile Gly Pro Pro Glu Ser Ile
 152 20 25 30
 153 tgg gtg acg ccg gga gaa gcc tcc ctc atc atc agg ttc tcc tct ccc 145
 154 Trp Val Thr Pro Gly Glu Ala Ser Leu Ile Ile Arg Phe Ser Ser Pro
 155 35 40 45
 156 ttc gac gtc cct ccc aac ctg ggc tat ttc cag tac tat gtc cat tay 193
 157 Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His Xaa
 158 50 55 60
 159 tgg gaa aag gcg gga atc caa aag gtt aaa ggt cct ttc aag agc aac 241
 160 Trp Glu Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Lys Ser Asn
 161 65 70 75 80
 162 tcc atc gtg ttg gat ggc ttg aga ccc tta aga gaa tac tgt tta caa 289
 163 Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu Gln
 164 85 90 95
 165 gtg aag gcg cat ctc ttt cgc aca tcc tgc aac acc tct agg ccc ggc 337
 166 Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro Gly
 167 100 105 110
 168 cgc tta agc aac ata act tgc tac gaa aca atg atg gat gcc act acg 385
 169 Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr Thr
 170 115 120 125
 171 aag ctt caa caa gtc atc ctc atc gcc gtg gga gtc ttt ctg tcg ctg 433
 172 Lys Leu Gln Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser Leu
 173 130 135 140
 174 gcg gcg ctg gcg ggg ggc tgt ttc ttc ctg gtg ctg aga tac aaa ggc 481
 175 Ala Ala Leu Ala Gly Gly Cys Phe Phe Leu Val Leu Arg Tyr Lys Gly
 176 145 150 155 160
 177 ctg gtg aaa tac tgg ttt cac tct ccg cca agc atc cca tca caa atc 529
 178 Leu Val Lys Tyr Trp Phe His Ser Pro Pro Ser Ile Pro Ser Gln Ile
 179 165 170 175
 180 gaa gag tat ctg aag gac ccg agc cag cct atc cta gag gcc ctg gac 577
 181 Glu Glu Tyr Leu Lys Asp Pro Ser Gln Pro Ile Leu Glu Ala Leu Asp
 182 180 185 190
 183 aag gac acg tca cca aca gat gat gcc tgg gac ttg gtg tct gtt gtt 625
 184 Lys Asp Thr Ser Pro Thr Asp Asp Ala Trp Asp Leu Val Ser Val Val
 185 195 200 205
 186 gca ttt cca gca aag gag caa gaa gat gtt ccc caa agc act ttg acc 673
 187 Ala Phe Pro Ala Lys Glu Gln Glu Asp Val Pro Gln Ser Thr Leu Thr
 188 210 215 220
 189 caa aac tct ggt gcg gtc tgc tagcctgtgg ggtaaggct ctgagccgag 724
 190 Gln Asn Ser Gly Ala Val Cys
 191 225 230
 192 gaagctgctg atgtccatgt cagcaactta tggaatccgg tcctccattt tcctgtcccc 784
 193 aaaaggcccg tcaagtgcctg tgaagatgta acgggtctca tggggcgcac aagcttattg 844
 194 attttttctt tcaaactaag agtttctaa tcatacgcgt ttttagaata attctacaga 904

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Input Set: I265540A.RAW

195 tatgtcccg aaagattaag atttcttta aacactaaaa agacatgtaa ttatttgtta 964
 196 gcaaatggc gtctggcacg cctctgacac ttttcgtca gcagccagga cacgagggcc 1024
 197 cctccttgcat gaagccccctc gggcagacca tgtcacctgt cccagcctgc cccaagaagg 1084
 198 gacattaagt gcccttctt catatccaaa cacctggctt gaaatgtgat tagccctgtta 1144
 199 aatagttca cagagattaa gcctttttt cccccaagtt aggaataaaaa gactataatt 1204
 200 aacttttaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1244
 201 <210> SEQ ID NO 4
 202 <211> LENGTH: 231
 203 <212> TYPE: PRT
 204 <213> ORGANISM: primate
 205 <220> FEATURE:
 206 <221> NAME/KEY: misc_feature
 207 <222> LOCATION: Xaa at residue 64
 208 <223> OTHER INFORMATION: Xaa translated amino acid depends on corresponding codon
 209 <400> SEQUENCE: 4
 Arg Val Asp Pro Arg Val Arg Leu Val Ser Pro Trp Leu Thr Val Pro
 1 5 10 15
 Trp Phe Leu Ser Cys Trp Asn Val Thr Ile Gly Pro Pro Glu Ser Ile
 20 25 30
 Trp Val Thr Pro Gly Glu Ala Ser Leu Ile Ile Arg Phe Ser Ser Pro
 35 40 45
 Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His Xaa
 50 55 60
 Trp Glu Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Lys Ser Asn
 65 70 75 80
 Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu Gln
 85 90 95
 Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro Gly
 100 105 110
 Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr Thr
 115 120 125
 Lys Leu Gln Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser Leu
 130 135 140
 Ala Ala Leu Ala Gly Gly Cys Phe Phe Leu Val Leu Arg Tyr Lys Gly
 145 150 155 160
 Leu Val Lys Tyr Trp Phe His Ser Pro Pro Ser Ile Pro Ser Gln Ile
 165 170 175
 Glu Glu Tyr Leu Lys Asp Pro Ser Gln Pro Ile Leu Glu Ala Leu Asp
 180 185 190
 Lys Asp Thr Ser Pro Thr Asp Asp Ala Trp Asp Leu Val Ser Val Val
 195 200 205
 Ala Phe Pro Ala Lys Glu Gln Glu Asp Val Pro Gln Ser Thr Leu Thr
 210 215 220
 Gln Asn Ser Gly Ala Val Cys
 225 230
 240 <210> SEQ ID NO 5
 241 <211> LENGTH: 337
 242 <212> TYPE: PRT
 243 <213> ORGANISM: primate
 244 <400> SEQUENCE: 5

Input Set: I265540A.RAW

Line	? Error/Warning	Original Text
52	W "N" or "Xaa" used: Feature required	ggg atg gag atc ncc aaa nat ggc ttc cac c
89	W "N" or "Xaa" used: Feature required	cttcatccct tnggtccnaa gttttctcat ctgtaatg
117	W "N" or "Xaa" used: Feature required	Ile Xaa Lys Xaa Gly Phe His Leu Val Ile G
119	W "N" or "Xaa" used: Feature required	Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp X
125	W "N" or "Xaa" used: Feature required	Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe S
127	W "N" or "Xaa" used: Feature required	Xaa Val Gln Gly Glu Ala Ile Pro Leu Val L
216	W "N" or "Xaa" used: Feature required	Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe G

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821-1.825 for the following reason(s):

- 1. This application clearly fails to comply with the requirements of 37 CFR 1.821-1.825. Applicant's attention is directed to these regulations, published at 114 FR 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c).
- 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(e).
- 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached copy of marked-up "Raw Sequence Listing."
- 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).
- 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).
- 7. Other: _____

Applicant must provide:

- An initial or substitute computer readable form (CRF) copy of the "Sequence Listing"
- An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification
- A statement that the content of the paper and computer readable copies are the same, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)

For questions regarding compliance with these requirements, please contact:

For Rules Interpretation, call (703) 308-1123

For CRF submission help, call (703) 308-4212

For PatentIn software help, call (703) 557-0400

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